

#5

RAW SEQUENCE LISTING

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Application Serial Number: 101523,503
Source: PCT
Date Processed by STIC: 2-17-05

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PATENT APPLICATION: US/10/523,503

DATE: 02/17/2005
TIME: 11:21:43

Input Set : A:\16313236.app
Output Set: N:\CRF4\02172005\J523503.raw

3 <110> APPLICANT: BASF PLANT SCIENCE GMBH
 5 <120> TITLE OF INVENTION: SUGAR AND LIPID METABOLISM REGULATORS IN PLANTS IV
 7 <130> FILE REFERENCE: 16313-0236
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/523,503
 C--> 10 <141> CURRENT FILING DATE: 2005-02-02
 12 <150> PRIOR APPLICATION NUMBER: US 60/400,803
 13 <151> PRIOR FILING DATE: 2002-08-02
 15 <160> NUMBER OF SEQ ID NOS: 163
 17 <170> SOFTWARE: PatentIn version 3.2
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 20 <211> LENGTH: 300
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Arabidopsis thaliana
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 29 tgcgggtggaa gatgcaaagg tagatgcgcg aaatcgctga gccaaatct gtgttgaga 180
 31 gcatgcaaca gctgttgtta ccgctgcaac tgtgtgccac caggcaccgc cggaaaccac 240
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 38 <212> TYPE: PRT
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 47 20 25 30
 50 Gly Glu Gly Val Val Lys Ile Asp Cys Gly Gly Arg Cys Lys Gly Arg
 51 35 40 45
 54 Cys Ser Lys Ser Ser Arg Pro Asn Leu Cys Leu Arg Ala Cys Asn Ser
 55 50 55 60
 58 Cys Cys Tyr Arg Cys Asn Cys Val Pro Pro Gly Thr Ala Gly Asn His
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 66 Lys Cys Pro
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 73 <213> ORGANISM: Arabidopsis thaliana
 75 <400> SEQUENCE: 3
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 80 ggagacccaa cactctactc gtgtttcgt acaacacaag tctcttca agctgttct 180
 82 gattctttc tctccaacaa gttccatggg tactcttcgta ccgtcggtct tccccaaagct 240
 84 cgaaggc aa tagcagagta tctatcggt gatctccat acaaactt acaggatgat 300
 86 gtgttatca catcgggtt caccgaagcg atcgatgtg cattgtcgat gtttagctcg 360
 88 cccaggcata atatacttcc tccaaggcct gggttccaa tctatgaact ctgtgctaag 420
 90 tttagacacc ttgaagttcg ctacgtcgat cttcttccgg aaaatggatg ggagatcgat 480
 92 ctgtatgctg tcgaggcctc tgacgacgaa aacacgggtt cttgggttataaaccct 540
 94 ggttaatcctt gcggaaatgt ctatagctac cagcattga tgaagattgc ggaatcgccg 600
 96 aaaaaactag gggttctt gattgctgat gaggttacg gtcatcttc ttttggtagc 660
 98 aaaccgttgc tgccaatggg tgggttttggatcttattgttctc tcttgctct 720
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 102 tctgggttctt ttaaggaccc taagatcatt gagaggttta agaaatactt tgatattctt 840
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 112 tttagcttaggg aagaatcagt catccttctt cctgggaccg cgggtgggct gaagaactgg 1140
 114 ctgaggataa cgttgcagc agatgcaact tcgattgaag aagctttaa aaggatcaaa 1200
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 133 Lys Arg Val Ile Ser Leu Gly Met Gly Asp Pro Thr Leu Tyr Ser Cys
 134 35 40 45
 137 Phe Arg Thr Thr Gln Val Ser Leu Gln Ala Val Ser Asp Ser Leu Leu
 138 50 55 60
 141 Ser Asn Lys Phe His Gly Tyr Ser Pro Thr Val Gly Leu Pro Gln Ala
 142 65 70 75 80
 145 Arg Arg Ala Ile Ala Glu Tyr Leu Ser Arg Asp Leu Pro Tyr Lys Leu
 146 85 90 95
 149 Ser Gln Asp Asp Val Phe Ile Thr Ser Gly Cys Thr Gln Ala Ile Asp
 150 100 105 110
 153 Val Ala Leu Ser Met Leu Ala Arg Pro Arg Ala Asn Ile Leu Leu Pro
 154 115 120 125
 157 Arg Pro Gly Phe Pro Ile Tyr Glu Leu Cys Ala Lys Phe Arg His Leu
 158 130 135 140
 161 Glu Val Arg Tyr Val Asp Leu Leu Pro Glu Asn Gly Trp Glu Ile Asp
 162 145 150 155 160
 165 Leu Asp Ala Val Glu Ala Leu Ala Asp Glu Asn Thr Val Ala Leu Val
 166 165 170 175
 169 Val Ile Asn Pro Gly Asn Pro Cys Gly Asn Val Tyr Ser Tyr Gln His
 170 180 185 190

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 174 195 200 205
 177 Ala Asp Glu Val Tyr Gly His Leu Ala Phe Gly Ser Lys Pro Phe Val
 178 210 215 220
 181 Pro Met Gly Val Phe Gly Ser Ile Val Pro Val Leu Thr Leu Gly Ser
 182 225 230 235 240
 185 Leu Ser Lys Arg Trp Ile Val Pro Gly Trp Arg Leu Gly Trp Phe Val
 186 245 250 255
 189 Thr Thr Asp Pro Ser Gly Ser Phe Lys Asp Pro Lys Ile Ile Glu Arg
 190 260 265 270
 193 Phe Lys Lys Tyr Phe Asp Ile Leu Gly Gly Pro Ala Thr Phe Ile Gln
 194 275 280 285
 197 Ala Ala Val Pro Thr Ile Leu Glu Gln Thr Asp Glu Ser Phe Phe Lys
 198 290 295 300
 201 Lys Thr Leu Asn Ser Leu Lys Asn Ser Ser Asp Ile Cys Cys Asp Trp
 202 305 310 315 320
 205 Ile Lys Glu Ile Pro Cys Ile Asp Ser Ser His Arg Pro Glu Gly Ser
 206 325 330 335
 209 Met Ala Met Met Val Lys Leu Asn Leu Ser Leu Leu Glu Asp Val Ser
 210 340 345 350
 213 Asp Asp Ile Asp Phe Cys Phe Lys Leu Ala Arg Glu Glu Ser Val Ile
 214 355 360 365
 217 Leu Leu Pro Gly Thr Ala Val Gly Leu Lys Asn Trp Leu Arg Ile Thr
 218 370 375 380
 221 Phe Ala Ala Asp Ala Thr Ser Ile Glu Glu Ala Phe Lys Arg Ile Lys
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 239 ccatctgaag ataaaaacgac gactgttgg ctaactaaaa tcaaacggtc cggtaaaaat 180
 241 tattgggcta aagtttagaga gactttggat cgtggacagt cccacttctt tcctccgaac 240
 243 acatatttta ccggaaagaa tgatgcgcgg atgggagccg gtaaaaatat gaaagaggcg 300
 245 gcgacgagga gctttgagca tagcaaagcg acggtgagg aagctgctag atcagcggca 360
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 253 <211> LENGTH: 152
 254 <212> TYPE: PRT
 255 <213> ORGANISM: Arabidopsis thaliana
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 262 Phe Ser Ile Phe Phe Leu Phe Val Leu Ser Val Asn Val Ser Ala

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271	50	55	60	
274	Val Arg Glu Thr Leu Asp Arg Gly Gln Ser His Phe Phe Pro Pro Asn			
275	65	70	75	80
278	Thr Tyr Phe Thr Gly Lys Asn Asp Ala Pro Met Gly Ala Gly Glu Asn			
279	85	90	95	
282	Met Lys Glu Ala Ala Thr Arg Ser Phe Glu His Ser Lys Ala Thr Val			
283	100	105	110	
286	Glu Glu Ala Ala Arg Ser Ala Ala Glu Val Val Ser Asp Thr Ala Glu			
287	115	120	125	
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312	ctggcttaca cagaattcgg aatccctaga gacgaagcca agttcaagat cataaacatc	300		
314	cacggcttcg attcttgat gcgagactcg catttcgcca atttcttatac gccggcttct	360		
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318	cctaacctga atgggtcacc aagaagcata gcattggata tagaagagct tgctgatggg	480		
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336	tggaatggcg atgaggataa gtttgtCCA gtaaagctt aacggatgt cgctcaaag	1020		
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355 Arg Thr His Thr Arg Asn Asn Thr Gln Gln Ser Ser Ser Ser Gly Tyr
 356 20 25 30
 359 Leu Lys Thr Leu Leu Leu Val Thr Phe Val Gly Val Leu Ala Trp Val
 360 35 40 45
 363 Tyr Gln Thr Ile Gln Pro Pro Pro Ala Lys Ile Val Gly Ser Pro Gly
 364 50 55 60
 367 Gly Pro Thr Val Thr Ser Pro Arg Ile Lys Leu Arg Asp Gly Arg His
 368 65 70 75 80
 371 Leu Ala Tyr Thr Glu Phe Gly Ile Pro Arg Asp Glu Ala Lys Phe Lys
 372 85 90 95
 375 Ile Ile Asn Ile His Gly Phe Asp Ser Cys Met Arg Asp Ser His Phe
 376 100 105 110
 379 Ala Asn Phe Leu Ser Pro Ala Leu Val Glu Glu Leu Arg Ile Tyr Ile
 380 115 120 125
 383 Val Ser Phe Asp Arg Pro Gly Tyr Gly Glu Ser Asp Pro Asn Leu Asn
 384 130 135 140
 387 Gly Ser Pro Arg Ser Ile Ala Leu Asp Ile Glu Glu Leu Ala Asp Gly
 388 145 150 155 160
 391 Leu Gly Leu Gly Pro Gln Phe Tyr Leu Phe Gly Tyr Ser Met Gly Gly
 392 165 170 175
 395 Glu Ile Thr Trp Ala Cys Leu Asn Tyr Ile Pro His Arg Leu Ala Gly
 396 180 185 190
 399 Ala Ala Leu Val Ala Pro Ala Ile Asn Tyr Trp Trp Arg Asn Leu Pro
 400 195 200 205
 403 Gly Asp Leu Thr Arg Glu Ala Phe Ser Leu Met His Pro Ala Asp Gln
 404 210 215 220
 407 Trp Ser Leu Arg Val Ala His Tyr Ala Pro Trp Leu Thr Tyr Trp Trp
 408 225 230 235 240
 411 Asn Thr Gln Lys Trp Phe Pro Ile Ser Asn Val Ile Ala Gly Asn Pro
 412 245 250 255
 415 Ile Ile Phe Ser Arg Gln Asp Met Glu Ile Leu Ser Lys Leu Gly Phe
 416 260 265 270
 419 Val Asn Pro Asn Arg Ala Tyr Ile Arg Gln Gln Gly Glu Tyr Val Ser
 420 275 280 285
 423 Leu His Arg Asp Leu Asn Val Ala Phe Ser Ser Trp Glu Phe Asp Pro
 424 290 295 300
 427 Leu Asp Leu Gln Asp Pro Phe Pro Asn Asn Asn Gly Ser Val His Val
 428 305 310 315 320
 431 Trp Asn Gly Asp Glu Asp Lys Phe Val Pro Val Lys Leu Gln Arg Tyr
 432 325 330 335
 435 Val Ala Ser Lys Leu Pro Trp Ile Arg Tyr His Glu Ile Ser Gly Ser
 436 340 345 350
 439 Gly His Phe Val Pro Phe Val Glu Gly Met Thr Asp Lys Ile Ile Lys
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 447 Val
 448 385
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VERIFICATION SUMMARY

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L:9 M:270 C: Current Application Number differs, Replaced Current Application Number

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date